In the Claims

1. (currently amended) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed by [a] an invertebrate host, produces an RNA having:

(a) homology to at least one target mRNA expressed by the host, and

(b) two fully complementary RNA regions which [are unrelated to] do not share sequence identity with any endogenous RNA in the host, and which are in proximity to the target mRNA [(a)],

wherein the [expressed] RNA expressed by the host reduces the expression of the target mRNA or any [substantially similar] endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

2. (currently amended) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed by [a] an invertebrate host, produces an RNA having:

(a) homology to at least one target mRNA expressed by the host,

(b) an RNA region [unrelated to] which does not share sequence identity with any endogenous RNA in the host and is located 5' to [(a)] the target mRNA, and

(c) the reverse complement of the RNA region which does not share sequence identity with any endogenous RNA in the host [in (b)] wherein the reverse complement is located 3' to [(a)] the target mRNA,

further wherein the [expressed] RNA expressed by the host reduces the expression of the target mRNA or any [substantially similar] endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

Claims 3 – 5 (withdrawn)

6. (currently amended) The recombinant construct of any of Claims 1-2 wherein the RNA region or regions which [are unrelated to] do not share sequence identity with any endogenous RNA in the host comprise a synthetic, non-naturally occurring RNA sequence.

7. (currently amended) The recombinant construct of any of Claims 1-2 wherein the RNA region or regions which [are unrelated to] do not share sequence identity with any endogenous RNA in the host do not comprise plant viral RNA.

8. (currently amended) A method for reducing expression of a target mRNA or any [substantially similar] endogenous mRNA that has at least 80% sequence identity with the RNA expressed by an invertebrate host based on the Clustal method of alignment, [which comprises] the method comprising:

(a) transforming a host with any of the recombinant constructs of Claims 1-2; and

(b) selecting hosts which have reduced expression of the target mRNA or any [substantially similar] endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

9. (currently amended) A method for reducing expression of a target mRNA or any [substantially similar] endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment, [which comprises] the method comprising:

(a) transforming a host with the recombinant construct of Claim 6; and

(b) selecting hosts which have reduced expression of the target mRNA or any [substantially similar] endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

10. (currently amended) A method for reducing expression of a target mRNA or any [substantially similar] endogenous mRNA that has at least 80% sequence identity with the RNA expressed by an invertebrate host based on the Clustal method of alignment, [which comprises] the method comprising:

(a) transforming a host with the recombinant construct of Claim 7; and

(b) selecting hosts which have reduced expression of the target mRNA or any [substantially similar] endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

11. (currently amended) An RNA comprising:

(a) homology to at least one target mRNA expressed by [a] an invertebrate host, and

(b) two fully complementary RNA regions which [are unrelated to] do not share sequence identity with any endogenous RNA in the host, and which are in proximity to [(a)] the target mRNA, wherein the RNA, when introduced into the host, reduces the expression of the target mRNA or any [substantially similar] endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

12. (currently amended) An RNA comprising:

(a) homology to at least one target mRNA expressed by [a] an invertebrate host,

(b) an RNA region [unrelated to] which does not share sequence identity with any endogenous RNA in the host and is located 5' to [(a)] the target mRNA, and

(c) the reverse complement of the RNA region which does not share sequence identity with any endogenous RNA in the host [in (b)] located 3' to [(a)] the target mRNA, wherein the RNA, when introduced into the host, reduces the expression of the target mRNA or any [substantially similar] endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

Claims 13 – 15 (withdrawn)

16. (currently amended) The RNA of any of Claims 11-12 wherein the RNA region or regions which [are unrelated to] do not share sequence identity with any endogenous RNA in the invertebrate host comprise a synthetic, non-naturally occurring RNA sequence.

17. (currently amended) The RNA of any of Claims 11-12 wherein the RNA region or regions which [are unrelated to] do not share sequence identity with any endogenous RNA in the invertebrate host do not comprise plant viral RNA.

18. (currently amended) A method for reducing expression of a target mRNA or any [substantially similar] endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment, [which comprises] the method comprising:

(a) introducing into a host any of the RNA of Claims 11-12; and

(b) selecting hosts which have reduced expression of the target mRNA or any [substantially similar] endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

19. (currently amended) A method for reducing expression of a target mRNA or any [substantially similar] endogenous mRNA that has at least 80% sequence identity with the RNA expressed by an invertebrate host based on the Clustal method of alignment, [which comprises] the method comprising:

(a) introducing into a host the recombinant construct of Claim 16; and

(b) selecting hosts which have reduced expression of the target mRNA or any [substantially similar] endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

Claims 20 – 44 (withdrawn)

45. (currently amended) The recombinant construct of Claims 1-2 wherein the DNA sequences encoding the two fully complementary RNA [sequences] regions are comprised within any of the sequences set forth in SEQ ID NOs: 12, 13, or 34.